

ABILITY OF A PROPIONATE PRODUCING CONSORTIUM TO PROMOTE RECOVERY FROM ANTIBIOTIC-ASSOCIATED GUT DYSBIOSIS

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Metabolic syndrome can result from obesity that is a growing public health concern. Propionate is a major fermentation product in our gut with several health benefits towards energy homeostasis. For instance, propionate is able to stimulate satiety-inducing hormones leading to lower energy intake and thus weight loss. In this study, the effect of a consortium of *Lactobacillus plantarum*, *Bacteroides thetaiotaomicron*, *Ruminococcus obeum*, *Coprococcus catus*, *Bacteroides vulgatus*, *Akkermansia muciniphila*, *Veillonella parvula* was studied for its potential to increase propionate concentrations in vitro. The mucosal simulator of the human intestinal microbial ecosystem (M-SHIME) was used to assess the total short chain fatty acid (SCFAs) and propionate production, as indicators of gut microbial functionality. Clindamycin was used to trigger dysbiosis, and the addition of the propionate-producing community aimed at raising the propionate levels in the in vitro system. SCFA was measured using gas chromatography method. Moreover, the effect of the consortium was assessed in the epithelial barrier function, membrane potential and mitochondrial activity in a triple co-culture model of Caco2, Ht29-MTX and HepG2 cells. Addition of the microbial consortium promoted recovery of the propionate levels following the supplementation with clindamycin, in comparison with controls. This consortium also showed a positive effect on epithelial barrier function, membrane potential and mitochondrial activity compared to the controls when its metabolites were not added on the cells. Our results indicate that, for a successful outcome, the next generation of “smart” probiotics must be designed taking into account the metabolic interactions among the members of the probiotic community.